

70
0328

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/931,071

DATE: 03/28/2002

TIME: 15:51:40

Input Set : A:\07334-335001.TXT

Output Set: N:\CRF3\03282002\I931071.raw

4 <110> APPLICANT: Bertin, John
 5 Alnemri, Emad S.
 7 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
 8 PROTEIN FAMILY AND USES THEREOF
 11 <130> FILE REFERENCE: 07334-335001
 13 <140> CURRENT APPLICATION NUMBER: 09/931,071
 C--> 14 <141> CURRENT FILING DATE: 2002-03-18
 16 <150> PRIOR APPLICATION NUMBER: 09/428,252
 17 <151> PRIOR FILING DATE: 1999-10-27
 19 <160> NUMBER OF SEQ ID NOS: 11
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 5444
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (523)...(4809)
 32 <400> SEQUENCE: 1

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35 gcagctcaag ggttgatctc aggagtccag gacccaggag agggagaat ctgaggaaca	180
36 cagaacagtg agcgttgccc acaccccatc tcccgtcacc acatctcccc tcacccctcac	240
37 cctccctgcc tggccctgga ccccatccca ggacctccct atcagctgac ttcttccagt	300
38 gtcttgacag cccctctggg ctccctccctc ccctggcttt tctaccact cccctctat	360
39 cggcgtctat ctgtagggtgc cctgggattt ataaaactgg gttccgaatg ctgaataaga	420
40 gacggttaaga gccaaaggcaa aggacagcac tgttctctgc ctgcctgata cctcaccac	480
41 ctgggaacat cccccagaca cctctttaac tccgggacag ag atg gct ggc gga	534
42 Met Ala Gly Gly	
43 1	
45 gcc tgg ggc cgc ctg gcc tgt tac ttg gag ttc ctg aag aag gag gag	582
46 Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu Lys Lys Glu Glu	
47 5 10 15 20	
49 ctg aag gag ttc cag ctt ctg ctc gcc aat aaa gcg cac tcc agg agc	630
50 Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala His Ser Arg Ser	
51 25 30 35	
53 tct tcg ggt gag aca ccc gct cag cca gag aag acg agt ggc atg gag	678
54 Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr Ser Gly Met Glu	
55 40 45 50	
57 gtg gcc tcg tac ctg gtg gct cag tat ggg gag cag cgg gcc tgg gac	726
58 Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln Arg Ala Trp Asp	
59 55 60 65	
61 cta gcc ctc cat acc tgg gag cag atg ggg ctg agg tca ctg tgc gcc	774

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62	Leu	Ala	Leu	His	Thr	Trp	Glu	Gln	Met	Gly	Leu	Arg	Ser	Leu	Cys	Ala	
63		70					75					80					
65	caa	gcc	cag	gaa	ggg	gca	ggc	cac	tct	ccc	tca	ttc	ccc	tac	agc	cca	822
66	Gln	Ala	Gln	Glu	Gly	Ala	Gly	His	Ser	Pro	Ser	Phe	Pro	Tyr	Ser	Pro	
67	85					90				95						100	
69	agt	gaa	ccc	cac	ctg	ggg	tct	ccc	agc	caa	ccc	acc	tcc	acc	gca	gtg	870
70	Ser	Glu	Pro	His	Leu	Gly	Ser	Pro	Ser	Gln	Pro	Thr	Ser	Thr	Ala	Val	
71				105						110					115		
73	cta	atg	ccc	tgg	atc	cat	gaa	ttg	ccg	gcg	ggg	tgc	acc	cag	ggc	tca	918
74	Leu	Met	Pro	Trp	Ile	His	Glu	Leu	Pro	Ala	Gly	Cys	Thr	Gln	Gly	Ser	
75				120					125					130			
77	gag	aga	agg	gtt	ttg	aga	cag	ctg	cct	gac	aca	tct	gga	cgc	cgc	tgg	966
78	Glu	Arg	Arg	Val	Leu	Arg	Gln	Leu	Pro	Asp	Thr	Ser	Gly	Arg	Arg	Trp	
79			135				140						145				
81	aga	gaa	atc	tct	gcc	tca	ctc	ctc	tac	caa	gct	ctt	cca	agc	tcc	cca	1014
82	Arg	Glu	Ile	Ser	Ala	Ser	Leu	Leu	Tyr	Gln	Ala	Leu	Pro	Ser	Ser	Pro	
83		150					155					160					
85	gac	cat	gag	tct	cca	agc	cag	gag	tca	ccc	aac	gcc	ccc	aca	tcc	aca	1062
86	Asp	His	Glu	Ser	Pro	Ser	Gln	Glu	Ser	Pro	Asn	Ala	Pro	Thr	Ser	Thr	
87	165				170					175						180	
89	gca	gtg	ctg	ggg	agc	tgg	gga	tcc	cca	cct	cag	ccc	agc	cta	gca	ccc	1110
90	Ala	Val	Leu	Gly	Ser	Trp	Gly	Ser	Pro	Pro	Gln	Pro	Ser	Leu	Ala	Pro	
91				185						190					195		
93	aga	gag	cag	gag	gct	cct	ggg	acc	caa	tgg	cct	ctg	gat	gaa	acg	tca	1158
94	Arg	Glu	Gln	Glu	Ala	Pro	Gly	Thr	Gln	Trp	Pro	Leu	Asp	Glu	Thr	Ser	
95			200						205					210			
97	gga	att	tac	tac	aca	gaa	atc	aga	gaa	aga	gag	aga	gag	aaa	tca	gag	1206
98	Gly	Ile	Tyr	Tyr	Thr	Glu	Ile	Arg	Glu	Arg	Glu	Arg	Glu	Lys	Ser	Glu	
99		215					220						225				
101	aaa	ggc	agg	ccc	cca	tgg	gca	gcg	gtg	gta	gga	acg	ccc	cca	cag	gcg	1254
102	Lys	Gly	Arg	Pro	Pro	Trp	Ala	Ala	Val	Val	Gly	Thr	Pro	Pro	Gln	Ala	
103		230					235					240					
105	cac	acc	agc	cta	cag	ccc	cac	cac	cac	cca	tgg	gag	cct	tct	gtg	aga	1302
106	His	Thr	Ser	Leu	Gln	Pro	His	His	His	Pro	Trp	Glu	Pro	Ser	Val	Arg	
107	245				250					255						260	
109	gag	agc	ctc	tgt	tcc	aca	tgg	ccc	tgg	aaa	aat	gag	gat	ttt	aac	caa	1350
110	Glu	Ser	Leu	Cys	Ser	Thr	Trp	Pro	Trp	Lys	Asn	Glu	Asp	Phe	Asn	Gln	
111				265						270					275		
113	aaa	ttc	aca	cag	ctg	cta	ctt	cta	caa	aga	cct	cac	ccc	aga	agc	caa	1398
114	Lys	Phe	Thr	Gln	Leu	Leu	Leu	Leu	Gln	Arg	Pro	His	Pro	Arg	Ser	Gln	
115			280						285					290			
117	gat	ccc	ctg	gtc	aag	aga	agc	tgg	cct	gat	tat	gtg	gag	gag	aat	cga	1446
118	Asp	Pro	Leu	Val	Lys	Arg	Ser	Trp	Pro	Asp	Tyr	Val	Glu	Glu	Asn	Arg	
119		295					300						305				
121	gga	cat	tta	att	gag	atc	aga	gac	tta	ttt	ggc	cca	ggc	ctg	gat	acc	1494
122	Gly	His	Leu	Ile	Glu	Ile	Arg	Asp	Leu	Phe	Gly	Pro	Gly	Leu	Asp	Thr	
123		310					315					320					
125	caa	gaa	cct	cgc	ata	gtc	ata	ctg	cag	ggg	gct	gct	gga	att	ggg	aag	1542
126	Gln	Glu	Pro	Arg	Ile	Val	Ile	Leu	Gln	Gly	Ala	Ala	Gly	Ile	Gly	Lys	

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127	325		330		335		340	
129	tca	aca	ctg	gcc	agg	cag	gtg	aag
130	Ser	Thr	Leu	Ala	Arg	Gln	Val	Lys
131				345		350		355
133	tat	ggg	gac	cgc	ttc	cag	cat	gtc
134	Tyr	Gly	Asp	Arg	Phe	Gln	His	Val
135				360		365		370
137	gcc	cag	tcc	aag	gtg	gtg	agt	ctc
138	Ala	Gln	Ser	Lys	Val	Val	Ser	Leu
139				375		380		385
141	aca	gcc	act	ccg	gct	ccc	att	aga
142	Thr	Ala	Thr	Pro	Ala	Pro	Ile	Arg
143				390		395		400
145	ctg	ctc	ttc	atc	ctc	gat	ggt	gta
146	Leu	Leu	Phe	Ile	Leu	Asp	Gly	Val
147	405			410		415		420
149	gag	ccg	agt	tct	gag	ctc	tgt	ctg
150	Glu	Pro	Ser	Ser	Glu	Leu	Cys	Leu
151				425		430		435
153	gat	gca	ctg	ctg	ggc	agt	ttg	ctg
154	Asp	Ala	Leu	Leu	Gly	Ser	Leu	Leu
155				440		445		450
157	tcc	ttc	ctg	atc	acg	gct	cgg	acc
158	Ser	Phe	Leu	Ile	Thr	Ala	Arg	Thr
159				455		460		465
161	tct	ttg	gag	cag	gca	cgt	tgg	gta
162	Ser	Leu	Glu	Gln	Ala	Arg	Trp	Val
163				470		475		480
165	agc	agg	aag	gaa	tat	ttc	tac	aga
166	Ser	Arg	Lys	Glu	Tyr	Phe	Tyr	Arg
167	485			490		495		500
169	att	aga	gcc	ttt	agg	ttg	gtc	aaa
170	Ile	Arg	Ala	Phe	Arg	Leu	Val	Lys
171				505		510		515
173	tgt	ctt	gtg	ccc	tgg	gtg	tcc	tgg
174	Cys	Leu	Val	Pro	Trp	Val	Ser	Trp
175				520		525		530
177	cag	atg	aag	cgg	aag	gaa	aaa	ctc
178	Gln	Met	Lys	Arg	Lys	Glu	Lys	Leu
179				535		540		545
181	acc	ctc	tgt	cta	cat	tac	ctt	gcc
182	Thr	Leu	Cys	Leu	His	Tyr	Leu	Ala
183				550		555		560
185	gga	ccc	cag	ctc	aga	gac	ctc	tgc
186	Gly	Pro	Gln	Leu	Arg	Asp	Leu	Cys
187	565			570		575		580
189	caa	aaa	aag	acc	ctt	ttc	agt	cca
190	Gln	Lys	Lys	Thr	Leu	Phe	Ser	Pro
191				585		590		595

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193	gat	ggg	gcc	atc	atc	tcc	acc	ttc	ttg	aag	atg	ggt	att	ctt	caa	gag	2358
194	Asp	Gly	Ala	Ile	Ile	Ser	Thr	Phe	Leu	Lys	Met	Gly	Ile	Leu	Gln	Glu	
195				600					605					610			
197	cac	ccc	atc	cct	ctg	agc	tac	agc	ttc	att	cac	ctc	tgt	ttc	caa	gag	2406
198	His	Pro	Ile	Pro	Leu	Ser	Tyr	Ser	Phe	Ile	His	Leu	Cys	Phe	Gln	Glu	
199				615				620						625			
201	ttc	ttt	gca	gca	atg	tcc	tat	gtc	ttg	gag	gat	gag	aag	ggg	aga	ggt	2454
202	Phe	Phe	Ala	Ala	Met	Ser	Tyr	Val	Leu	Glu	Asp	Glu	Lys	Gly	Arg	Gly	
203			630					635						640			
205	aaa	cat	tct	aat	tgc	atc	ata	gat	ttg	gaa	aag	acg	cta	gaa	gca	tat	2502
206	Lys	His	Ser	Asn	Cys	Ile	Ile	Asp	Leu	Glu	Lys	Thr	Leu	Glu	Ala	Tyr	
207	645					650					655					660	
209	gga	ata	cat	ggc	ctg	ttt	ggg	gca	tca	acc	aca	cgt	ttc	cta	ttg	ggc	2550
210	Gly	Ile	His	Gly	Leu	Phe	Gly	Ala	Ser	Thr	Thr	Arg	Phe	Leu	Leu	Gly	
211				665					670							675	
213	ctg	tta	agt	gat	gag	ggg	gag	aga	gag	atg	gag	aac	atc	ttt	cac	tgc	2598
214	Leu	Leu	Ser	Asp	Glu	Gly	Glu	Arg	Glu	Met	Glu	Asn	Ile	Phe	His	Cys	
215				680					685					690			
217	cgg	ctg	tct	cag	ggg	agg	aac	ctg	atg	cag	tgg	gtc	ccg	tcc	ctg	cag	2646
218	Arg	Leu	Ser	Gln	Gly	Arg	Asn	Leu	Met	Gln	Trp	Val	Pro	Ser	Leu	Gln	
219				695				700						705			
221	ctg	ctg	ctg	cag	cca	cac	tct	ctg	gag	tcc	ctc	cac	tgc	ttg	tac	gag	2694
222	Leu	Leu	Leu	Gln	Pro	His	Ser	Leu	Glu	Ser	Leu	His	Cys	Leu	Tyr	Glu	
223			710				715					720					
225	act	cgg	aac	aaa	acg	ttc	ctg	aca	caa	gtg	atg	gcc	cat	ttc	gaa	gaa	2742
226	Thr	Arg	Asn	Lys	Thr	Phe	Leu	Thr	Gln	Val	Met	Ala	His	Phe	Glu	Glu	
227	725					730					735					740	
229	atg	ggc	atg	tgt	gta	gaa	aca	gac	atg	gag	ctc	tta	gtg	tgc	act	ttc	2790
230	Met	Gly	Met	Cys	Val	Glu	Thr	Asp	Met	Glu	Leu	Leu	Val	Cys	Thr	Phe	
231				745					750					755			
233	tgc	att	aaa	ttc	agc	cgc	cac	gtg	aag	aag	ctt	cag	ctg	att	gag	ggc	2838
234	Cys	Ile	Lys	Phe	Ser	Arg	His	Val	Lys	Lys	Leu	Gln	Leu	Ile	Glu	Gly	
235				760					765					770			
237	agg	cag	cac	aga	tca	aca	tgg	agc	ccc	acc	atg	gta	gtc	ctg	ttc	agg	2886
238	Arg	Gln	His	Arg	Ser	Thr	Trp	Ser	Pro	Thr	Met	Val	Val	Leu	Phe	Arg	
239				775				780						785			
241	tgg	gtc	cca	gtc	aca	gat	gcc	tat	tgg	cag	att	ctc	ttc	tcc	gtc	ctc	2934
242	Trp	Val	Pro	Val	Thr	Asp	Ala	Tyr	Trp	Gln	Ile	Leu	Phe	Ser	Val	Leu	
243			790				795					800					
245	aag	gtc	acc	aga	aac	ctg	aag	gag	ctg	gac	cta	agt	gga	aac	tcg	ctg	2982
246	Lys	Val	Thr	Arg	Asn	Leu	Lys	Glu	Leu	Asp	Leu	Ser	Gly	Asn	Ser	Leu	
247	805					810					815					820	
249	agc	cac	tct	gca	gtg	aag	agt	ctt	tgt	aag	acc	ctg	aga	cgc	cct	cgc	3030
250	Ser	His	Ser	Ala	Val	Lys	Ser	Leu	Cys	Lys	Thr	Leu	Arg	Arg	Pro	Arg	
251				825					830							835	
253	tgc	ctc	ctg	gag	acc	ctg	cgg	ttg	gct	ggc	tgt	ggc	ctc	aca	gct	gag	3078
254	Cys	Leu	Leu	Glu	Thr	Leu	Arg	Leu	Ala	Gly	Cys	Gly	Leu	Thr	Ala	Glu	
255				840					845					850			
257	gac	tgc	aag	gac	ctt	gcc	ttt	ggg	ctg	aga	gcc	aac	cag	acc	ctg	acc	3126

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258	Asp	Cys	Lys	Asp	Leu	Ala	Phe	Gly	Leu	Arg	Ala	Asn	Gln	Thr	Leu	Thr	
259			855					860					865				
261	gag	ctg	gac	ctg	agc	ttc	aat	gtg	ctc	acg	gat	gct	gga	gcc	aaa	cac	3174
262	Glu	Leu	Asp	Leu	Ser	Phe	Asn	Val	Leu	Thr	Asp	Ala	Gly	Ala	Lys	His	
263			870				875					880					
265	ctt	tgc	cag	aga	ctg	aga	cag	ccg	agc	tgc	aag	cta	cag	cga	ctg	cag	3222
266	Leu	Cys	Gln	Arg	Leu	Arg	Gln	Pro	Ser	Cys	Lys	Leu	Gln	Arg	Leu	Gln	
267	885					890				895					900		
269	ctg	gtc	agc	tgt	ggc	ctc	acg	tct	gac	tgc	tgc	cag	gac	ctg	gcc	tct	3270
270	Leu	Val	Ser	Cys	Gly	Leu	Thr	Ser	Asp	Cys	Cys	Gln	Asp	Leu	Ala	Ser	
271				905				910				915					
273	gtg	ctt	agt	gcc	agc	ccc	agc	ctg	aag	gag	cta	gac	ctg	cag	cag	aac	3318
274	Val	Leu	Ser	Ala	Ser	Pro	Ser	Leu	Lys	Glu	Leu	Asp	Leu	Gln	Gln	Asn	
275			920					925				930					
277	aac	ctg	gat	gac	gtt	ggc	gtg	cga	ctg	ctc	tgt	gag	ggg	ctc	agg	cat	3366
278	Asn	Leu	Asp	Asp	Val	Gly	Val	Arg	Leu	Leu	Cys	Glu	Gly	Leu	Arg	His	
279			935				940					945					
281	cct	gcc	tgc	aaa	ctc	ata	cgc	ctg	ggg	ctg	gac	cag	aca	act	ctg	agt	3414
282	Pro	Ala	Cys	Lys	Leu	Ile	Arg	Leu	Gly	Leu	Asp	Gln	Thr	Thr	Leu	Ser	
283		950				955				960							
285	gat	gag	atg	agg	cag	gaa	ctg	agg	gcc	ctg	gag	cag	gag	aaa	cct	cag	3462
286	Asp	Glu	Met	Arg	Gln	Glu	Leu	Arg	Ala	Leu	Glu	Gln	Glu	Lys	Pro	Gln	
287	965				970				975						980		
289	ctg	ctc	atc	ttc	agc	aga	cgg	aaa	cca	agt	gtg	atg	acc	cct	act	gag	3510
290	Leu	Leu	Ile	Phe	Ser	Arg	Arg	Lys	Pro	Ser	Val	Met	Thr	Pro	Thr	Glu	
291			985					990				995					
293	ggc	ctg	gat	acg	gga	gag	atg	agt	aat	agc	aca	tcc	tca	ctc	aag	cgg	3558
294	Gly	Leu	Asp	Thr	Gly	Glu	Met	Ser	Asn	Ser	Thr	Ser	Ser	Leu	Lys	Arg	
295			1000					1005				1010					
297	cag	aga	ctc	gga	tca	gag	agg	gcg	gct	tcc	cat	gtt	gct	cag	gct	aat	3606
298	Gln	Arg	Leu	Gly	Ser	Glu	Arg	Ala	Ala	Ser	His	Val	Ala	Gln	Ala	Asn	
299			1015				1020					1025					
301	ctc	aaa	ctc	ctg	gac	gtg	agc	aag	atc	ttc	cca	att	gct	gag	att	gca	3654
302	Leu	Lys	Leu	Leu	Asp	Val	Ser	Lys	Ile	Phe	Pro	Ile	Ala	Glu	Ile	Ala	
303		1030				1035				1040							
305	gag	gaa	agc	tcc	cca	gag	gta	gta	ccg	gtg	gaa	ctc	ttg	tgc	gtg	cct	3702
306	Glu	Glu	Ser	Ser	Pro	Glu	Val	Val	Pro	Val	Glu	Leu	Leu	Cys	Val	Pro	
307	1045				1050				1055						1060		
309	tct	cct	gcc	tct	caa	ggg	gac	ctg	cat	acg	aag	cct	ttg	ggg	act	gac	3750
310	Ser	Pro	Ala	Ser	Gln	Gly	Asp	Leu	His	Thr	Lys	Pro	Leu	Gly	Thr	Asp	
311			1065					1070				1075					
313	gat	gac	ttc	tgg	ggc	ccc	acg	ggg	cct	gtg	gct	act	gag	gta	gtt	gac	3798
314	Asp	Asp	Phe	Trp	Gly	Pro	Thr	Gly	Pro	Val	Ala	Thr	Glu	Val	Val	Asp	
315			1080					1085				1090					
317	aaa	gaa	aag	aac	ttg	tac	cga	gtt	cac	ttc	cct	gta	gct	ggc	tcc	tac	3846
318	Lys	Glu	Lys	Asn	Leu	Tyr	Arg	Val	His	Phe	Pro	Val	Ala	Gly	Ser	Tyr	
319			1095					1100				1105					
321	cgc	tgg	ccc	aac	acg	ggt	ctc	tgc	ttt	gtg	atg	aga	gaa	gcg	gtg	acc	3894
322	Arg	Trp	Pro	Asn	Thr	Gly	Leu	Cys	Phe	Val	Met	Arg	Glu	Ala	Val	Thr	

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date